SEQUENCE LISTING

<110> BESEME, Frederic

BLOND, Jean-Luc

BOUTON, Olivier

MANDRAND, Bernard

MALLET, Francois

PERRON, Herve

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<141> 1999-12-16

<150> PCT/FR98/01442

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<150> FR 97/08815

<151> 1997-07-07

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<221> misc_feature

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<222> (833)..(833)

<223> n = any nucleotide

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<211> 783

<212> DNA

<213> Artificial Sequence

<220>

<223> Consensus Sequence

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<221> misc_feature

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<223> n = any nucleotide

<220>

<221> misc_feature

<222> (515)..(515)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (563)..(563)

<223> n = any nucleotide

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rgscaacgaa cyccasgtca gagaayacga rgcttgccac catcttggaa gcggcctgct 720

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer or probe

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<210> 17

<211> 21

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<213> Artificial Sequence

<220>

<223> PCR primer or probe

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<210> 18

<211> 21

<212> DNA

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<220>

<223> PCR primer or probe

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<210> 19

<211> 24

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<220>

<223> PCR primer or probe

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<210> 21

<211> 22

<212> DNA

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<223> Probe or primer

<400> 24
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<223> Probe or primer

<400> 26
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<210> 27

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe or primer

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<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe or primer

<400> 28
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<210> 29

<211> 678

<212> DNA

<213> Artificial Sequence

<220>

<223> Ppol-MSRV probe

<220>

<221> misc_feature

<222> (594)..(594)

<223> n = any nucleotide

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tatatacact aattaaggaa actcagaaag ccaataccca tttagtaaga tggacacctg 480

aagcagaggc agctttccag gccgtaaaga acaccctaac ccaagcccca gtgttaagct 540

tgccagcggg gcaagacttt tctttctgtg tcacagaaaa aataggaata gctntaggag 600

tccttacaca ggtccgaggg accagcttgc aacccatggc atacctgagt aaggaaattg 660

atgtagtggc aaagggtt 678

<210> 30

<211> 536

<212> DNA

<213> Artificial Sequence

<220>

<223> Pgag-LB19 probe

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cgagagtttg gcaatctctg gtatctcagt caggtcaatg ataggatgac aacggaggaa 420

agagaacgat tccccacagg gcagcaggca gttcccagtg tagctcctca ttgggacaca 480

gaatcagaac atggagattg gtgccgcaga catttaaagc tttccccggg taccga 536

<210> 31

<211> 591

<212> DNA

<213> Artificial Sequence

<220>

<223> Penv-C15 probe

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cagctctaat attgttactc ctctttggac cctgtatctt taacctcctt gttaagtttg 540

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<210> 32

<211> 364

<212> DNA

<213> Artificial Sequence

<220>

<223> Ppro-E probe

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gacactggcg cagccttctc agtcttactt tcctgtccca gacaattgtc ctccagatct 180

gtcactatcc gaggggtcct aggacagcca gtcactacat acttctctca gccactaagt 240

tgtgactggg gaactttact cttttcacat gcttttctaa ttatgcctga aagccccact 300

cccttgttag ggagagacat tttagcaaaa gcaggggcca ttatacacct gaacaagctt 360

gaaa 364

<210> 33

<211> 538

<212> PRT

<213> Human

<400> 33

Met Gly Leu Pro Tyr His Ile Phe Leu Cys Ser Val Leu Ser Pro Cys
1 5 10 15

Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
20 25 30

Pro His Pro Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
35 40 45

Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
115 120 125

Val Lys Glu Val Ile Ser Gln Leu Thr Gly Val His Gly Thr Ser Ser
130 135 140

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Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145                 150                 155                 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
                165                 170                 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
            180                 185                 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
        195                 200                 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
    210                 215                 220

Ser Asn Val Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225                 230                 235                 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
                245                 250                 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
            260                 265                 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
        275                 280                 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
    290                 295                 300

Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
305                 310                 315                 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
                325                 330                 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
            340                 345                 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
        355                 360                 365
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Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Arg Asn Arg Arg
    370                 375                 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
385                 390                 395                 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
                405                 410                 415

Lys Val Glu Glu Ile Pro Asp Arg Ile Gln Arg Ile Ala Glu Glu Leu
            420                 425                 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Arg Trp Met Pro Trp Ile
        435                 440                 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
    450                 455                 460

Gly Pro Cys Ile Phe Asp Leu Leu Val Asn Phe Val Ser Ser Arg Ile
465                 470                 475                 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
                485                 490                 495

Ile Tyr Arg Arg Pro Leu Asp Arg Pro Ala Ser Pro Arg Ser Asp Val
            500                 505                 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
        515                 520                 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
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<210> 34

<211> 52

<212> PRT

<213> Human

<400> 34

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Met Glu Pro Lys Met Gln Ser Lys Thr Lys Ile Tyr Arg Arg Pro Leu
1               5                   10                  15
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Asp Arg Pro Ala Ser Pro Arg Ser Asp Val Asn Asp Ile Lys Gly Thr
20 25 30

Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro Leu Leu Arg Pro Asn Ser
35 40 45

Ala Gly Ser Ser
50

<210> 35

<211> 48

<212> PRT

<213> Human

<400> 35

Met Leu Met Thr Ser Lys Ala Pro Leu Leu Arg Lys Ser Gln Leu His
1 5 10 15

Asn Leu Tyr Tyr Ala Pro Ile Gln Gln Glu Ala Val Arg Ala Val Val
20 25 30

Gly Gln Pro Pro Gln Gln His Leu Gly Phe Pro Val Glu Met Gly Asp
35 40 45

<210> 36

<211> 20

<212> DNA

<213> Human

<400> 36
atccaaagtg gtgagtaata 20

<210> 37

<211> 20

<212> DNA

<213> Human

<400> 37
ctttttcag atgggaaacg 20

<210> 38

<211> 10

<212> DNA

<213> Human

<400> 38
atccmaagtg 10

<210> 39

<211> 20

<212> DNA

<213> Human

<400> 39
caggaggaaa gtaactaaaa 20

<210> 40

<211> 10

<212> DNA

<213> Human

<400> 40
atgggaaacg 10

<210> 41

<211> 20

<212> DNA

<213> Human

<400> 41
ccatccctag atacatcctg 20

<210> 42

<211> 20

<212> DNA

<213> Human

<400> 42
tctcttccag aatcgaagct 20

<210> 43

<211> 873

<212> DNA

<213> Human

<400> 43
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ttgcaactga gagacaggac tagctggatt tcctaggccg actaagaatc cctaagccta 120

gctgggaagg tgaccacgtc cacctttaaa cacggggctt gcaacttagc tcacacctga 180

ccaatcagag agctcactaa aatgctaatt aggcaaagac aggaggtaaa gaaatagcca 240

atcatctatt gcctgagagc acagcaggag ggacaacaat cgggatataa acccaggcat 300

tcgagctggc aacagcagcc ccccttgggg tcccttccct ttgtatggga gctgttttca 360

tgctatttca ctctattaaa tcttgcaact gcactcttct ggtccatgtt tcttacggct 420

cgagctgagc ttttgctcac cgtccaccac tgctgtttgc caccaccgca gacctgccgc 480

tgactcccat ccctctggat cctgcagggt gtccgctgtg ctcctgatcc agcgaggcgc 540

ccattgccgc tcccaattgg gctaaaggct tgccattgtt cctgcacggc taagtgcctg 600

ggtttgttct aattgagctg aacactagtc actgggttcc atggttctct tctgtgaccc 660

acggcttcta atagaactat aacacttacc acatggccca agattccatt ccttggaatc 720

cgtgaggcca agaactccag gtcagagaat acgaggcttg ccaccatctt ggaagcggcc 780

tgctaccatc ttggaagtgg ttcaccacca tcttgggagc tctgtgagca aggacccccc 840

ggtaacattt tggcaaccac gaacggacat cca 873

<210> 44

<211> 815

<212> DNA

<213> Human

<400> 44
tcgtcggcca acctccccaa cagcacttag gttttcctgt tgagatgggg gactgagaga 60

caggactagc tggatttcct aggctgacta agaatcccta agcctagctg ggaaggtgac 120

cacatccacc tttaaacacg gggcttgcaa cttagctcac acctgaccaa tcagagagct 180

cactaaaatg ctaattaggc aaagacagga ggtaaagaaa tagccaatca tctattgcct 240

gagagcacag caggagggac aatgatcggg atataaaccc aagtcttcga gccggcaacg 300

gcaacccccc ttgggtcccc tccctttgta tgggagctct gttttcatgc tatttcactc 360

tattaaatct tgcaactgca ctcttctggt ccatgtttct tacggcttga gctgagcttt 420

cgctcgccat ccaccactgc tgtttgccgc caccgcagac ccgccgctga ctcccatccc 480

tctggatcat gcagggtgtc cgctgtgctc ctgatccagc gaggcaccca ttgccgctcc 540

caatcgggct aaaggcttgc cattgttcct gcatggctaa gtgcctgggt tcatcctaat 600

tgagctgaac actagtcact gggttccatg gttctcttct gtgacccaca gcttctaata 660

gagctataac actcaccgca tggcccaagg ttccattcct tgaatccata aggccaagaa 720

ccccaggtca gagaacacga ggcttgccac catcttggga gctctgtgag caaggacccc 780

caagtaacac aaccatgagg gtgcaaatgc atggg 815

<210> 45

<211> 425

<212> DNA

<213> Human

<400> 45
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atccttaagc ctaggtggga aggtgaccac atccaccttt aaacacgggg cttgcaactt 180

agctcacacc tgaccaatca gagagctcac taaaatgcta attaggcaaa gacaggaggt 240

aaagaaatag ccaatcattt attgcctgag agcacagcag gagggacaat gatcgggata 300

taaacccaag ttttcgagcc ggcaacggca acccccctttg ggtcccctcc ctttgtatgg 360

gagctctgtt ttcatgctat ttcactctat taaatcttgc aactgcaaaa aaaaaaaaaa 420

aaaaa 425

<210> 46

<211> 427

<212> DNA

<213> Human

<400> 46

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atccctaagc ctagctggga aggtgaccac atccaccttt aaacacgggg cttgcaactt 180

agttcacacc tgaccaatca gagagctcac taaaatgcta attaggcaaa gacaggaggt 240

aaagaaatag ccaatcatct attgcatgag agcacagcag gagggacaat gatcgggata 300

taaacccaag tcttcgagcc ggcaacggca acccccctttg ggtcccctcc ctttgtatgg 360

gagctctgtt ttcatgctat ttcactctat taaatcttgc agctgcgaaa aaaaaaaaaa 420

aaaaaaa 427

<210> 47

<211> 600

<212> DNA

<213> Human

<400> 47

caacaatcgg gatataaacc caggcattcg agctggcaac agcagccccc ctttgggtcc 60

cttccctttg tatgggagct gttttcatgc tatttcactc tattaaatct tgcaactgca 120

ctcttctggt ccatgtttct tacggctcga gctgagcttt tgctcaccgt ccaccactgc 180

tgtttgccac caccgcagac ctgccgctga ctcccatccc tctggatcct gcagggtgtc 240

cgctgtgctc ctgatccagc gaagcgccca ttgccgctcc caattgggct aaaggcttgc 300

cattgttcct gcacggctaa gtgcctgggt ttgttctaat tgagctgaac actagtcact 360

gggttccatg gttctcttct gtgacccacg gcttctaata gaactataac acttaccaca 420

tggcccaaga ttccattcct tggaatccgt gaggccaaga actccaggtc agagaatacg 480

aagcttgcca ccatcttgga agcggcctgc taccatcttg gaagtggttc accaccatct 540

tgggagctct gtgagcaagg acccccccggt aacattttgg caaccacgaa cggacatcca 600

<210> 48

<211> 530

<212> DNA

<213> Human

<400> 48

atgggagctg ttttcatgct atttcactct attaaatctt gcaactgcac tcttctggtc 60

catgtttctt acggctcgag ctgagctttt gctcaccgtc caccactgct gtttgccacc 120

accgcagacc tgccgctgac tcccatccct ctggatcctg cagggtgtcc gctgtgctcc 180

tgatccagcg aagcgcccat tgccgctccc aattgggcta aaggcttgcc attgttcctg 240

cacggctaag tgcctgggtt tgttctaatt gagctgaaca ctagtcactg ggttccatgg 300

ttctcttctg tgacccacgg cttctaatag aactataaca cttaccacat ggcccaagat 360

tccattcctt ggaatccgtg aggccaacga actccaggtc agagaatacg aagcttgcca 420

ccatcttgga agcggcctgc taccatcttg gaagtggttc accaccatct tgggagctct 480

gtgagcaagg acccccccggt gacattttgg cgaccaccaa cggacatccc 530

<210> 49

<211> 486

<212> DNA

<213> Human

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<221> misc_feature

<222> (84)..(84)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (193)..(193)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (241)..(241)

<223> n = any nucleotide

<400> 49

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cactgctgtt tgccaccacc gcanacctgc cgctgactcc catccctctg gatcctgcag 120

ggtgtccgct gtgctcctga tccagcgagg cgcccattgc cgctcccaat tgggctaaag 180

gcttgccatt gtncctgcac ggctaagtgc ctgggtttgt tctaattgag ctgaacacta 240

ntcactgggt tccatggttc tcttctgtga cccacggctt ctaatagaac tataacactt 300

accacatggc ccaagattcc attccttgga atccgtgagg gcaagaactc caggtcagag 360

aatacgaggc ttgccaccat cttggaagcg gcctgctacc atcttggaag tggttcacca 420

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catcca 486

<210> 50

<211> 37

<212> PRT

<213> Human

<400> 50

Lys Ile Tyr Arg Arg Pro Leu Asp Arg Pro Ala Ser Pro Arg Ser Asp
1 5 10 15

Val Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln
20 25 30

Pro Leu Leu Arg Pro
35

<210> 51

<211> 35

<212> PRT

<213> Human

<400> 51

Met Thr Ser Lys Ala Pro Leu Leu Arg Lys Ser Gln Leu His Asn Leu
1 5 10 15

Tyr Tyr Ala Pro Ile Gln Gln Glu Ala Val Arg Ala Val Val Gly Gln
20 25 30

Pro Pro Gln
35

<210> 52

<211> 33

<212> PRT

<213> Rex PTLV-L

<400> 52

Arg Leu Tyr Asn Thr Leu Ser Leu Asp Ser Pro Pro Ser Pro Pro Lys
1 5 10 15

Glu Leu Pro Ala Pro Ser Arg Phe Ser Pro Pro Gln Pro Leu Leu Arg
20 25 30

Pro

<210> 53

<211> 35

<212> PRT

<213> Tat SIV-AGM

<400> 53

Val Thr Tyr His Ala Pro Arg Thr Arg Arg Lys Lys Ile Arg Ser Leu
1 5 10 15

Asn Leu Ala Pro Leu Gln His Gln Ser Ile Ser Thr Lys Trp Gly Arg
20 25 30

Asp Gly Gln
35